

*[Handwritten signature/initials]*

## I. AMENDMENTS

### IA. AMENDMENTS TO THE SPECIFICATION

Please enter the following amendments to the specification.

Please amend the paragraph beginning on page 8, line 9, as follows:

*B* In addition to the naturally occurring GST-3 protein, GST-3 polypeptides which vary from the naturally occurring GST-3 protein are also provided. By GST-3 polypeptide is meant an amino acid sequence encoded by an open reading frame (ORF) of the *GST-3* gene, described in greater detail below, including the full length GST-3 protein and fragments thereof, particularly biologically active fragments and/or fragments corresponding to functional domains, e.g. acceptor binding site (postulated to be the most 5' consensus region A (see experimental section *infra*), the donor binding site, e.g. VRYEDL (SEQ ID NO:09), and the like; and including fusions of the subject polypeptides to other proteins or parts thereof. Fragments of interest will typically be at least about 10 aa in length, usually at least about 50 aa in length, and may be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of amino acids that is identical to GST-3 of at least about 10 aa, and usually at least about 15 aa, and in many embodiments at least about 50 aa in length.

*37*  
Please amend the paragraph beginning on page ~~37~~, line 13, as follows:

*Am* Three cDNA clones which encode three different human homologs for C6ST/KSST have been obtained. The predicted GST proteins are type 2 membrane proteins 411, 477, and 386 amino acids in length, respectively. Each has a relatively short transmembrane domain and a short amino-terminal cytoplasmic tail. Table 2 ~~demonstrates~~ demonstrates the high homologies among the 3 human proteins and the chick CS6T/KSST. Overall homologies at the amino acid level ranged from 28% to 40% identity. Strikingly, there are three regions of 16 to 29 amino acids in which identity among the three GSTs ranged from 50-59% and similarity ranged from 65-94%. See Fig. 6. In Fig. 6 shows that all four of the sulfotransferases are type II transmembrane proteins with short cytoplasmic tails (TM). There are three regions (region A, B and C) in which identities among the human GSTs range from 50-59% and similarities range from 65 to 94%. The amino acid sequence for the regions are:

A: (T/S)XRSGSSF(V/F)G(Q/E)LFXQX(P/L)(D/E)VF(F/Y)L(F/Y/M)EP(L/V/A)(W/Y)HV SEQ ID  
NO:10

*hr* B: L(N/D)L(K/H)(V/I)(I/V)XLVRDPR(A/G)(V/I)(LAF) SEQ ID NO:11

C: PXXL(Q/K)XXY(L/M)(L/V)VRYEDL(A/V)XXP (SEQ ID NO:12)

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